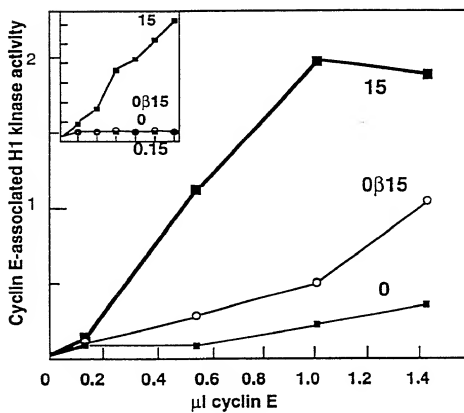


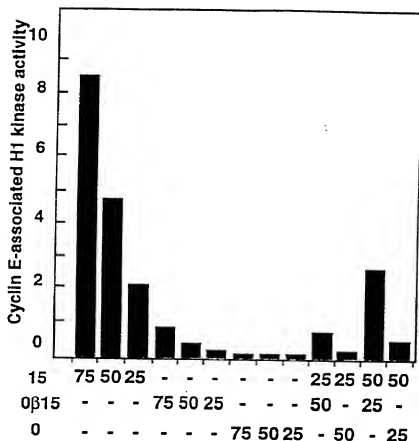
1/32

FIGURE 1A



2/32

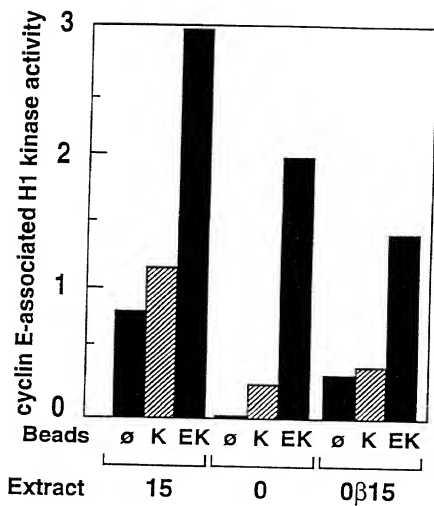
FIGURE 1B



00365018.054401

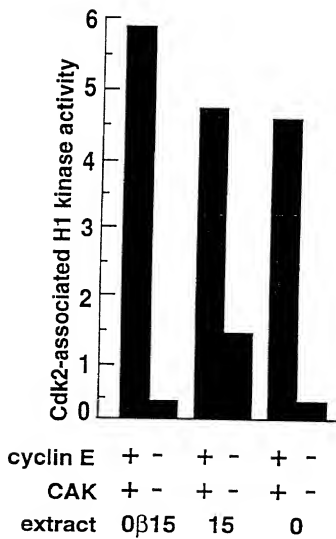
3/32

FIGURE 2A



4/32

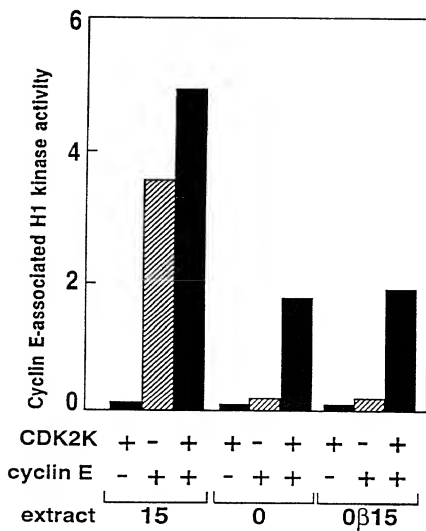
FIGURE 2B



104250\*81059860

5/32

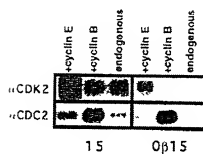
FIGURE 2C



104250' 81059860

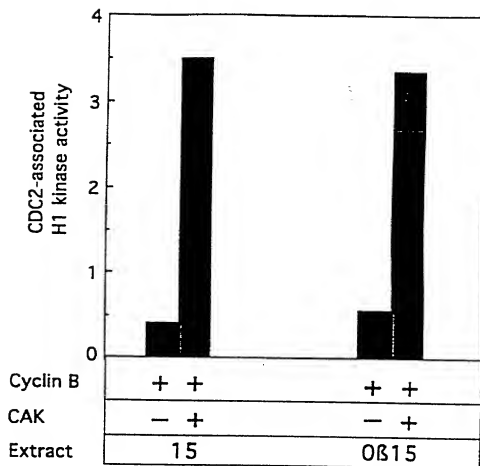
6/32

FIGURE 3A



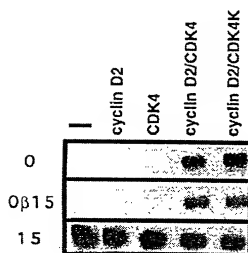
7/32

FIGURE 3B



8/32

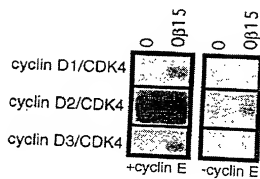
FIGURE 4A





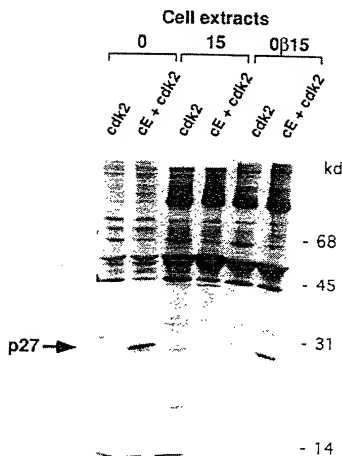
9/32

FIGURE 4B



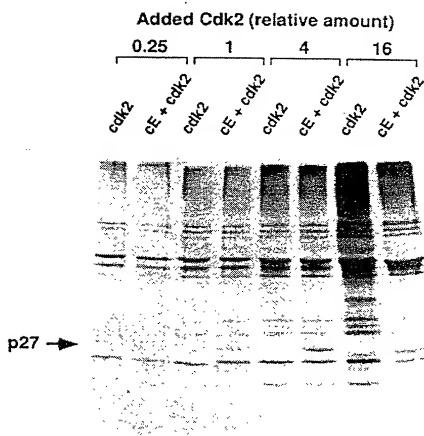
10/32

FIGURE 5A



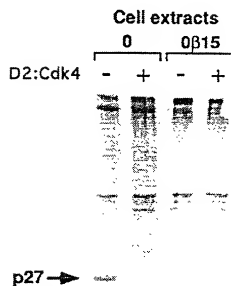
11/32

FIGURE 5B



12/32

FIGURE 5C



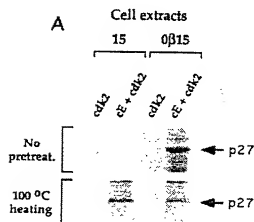
13/32

FIGURE 5D



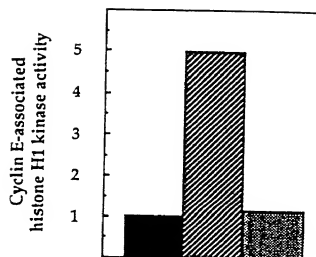
14/32

FIGURE 6A



15/32

FIGURE 6B



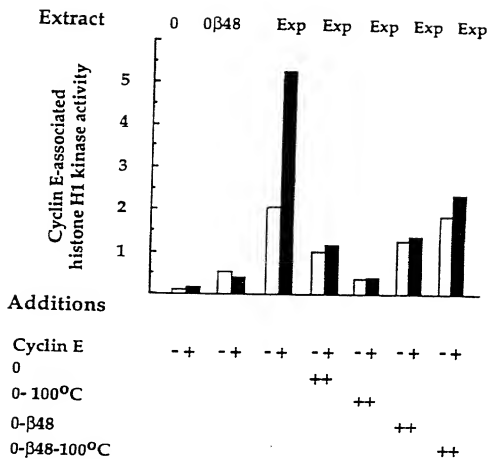
Additions:

100°C-Heated	-	-	+
Exp. cell extract	-	-	+
Cyclin E	-	+	+

09865018.05401  
104250.8105860

16/32

FIGURE 6C

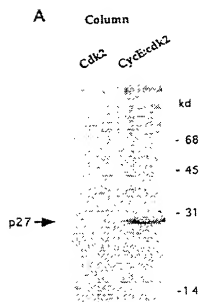


104250.8105960



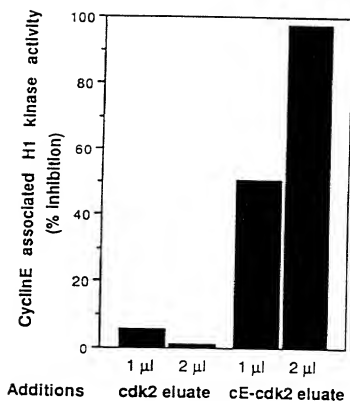
17/32

## FIGURE 7A



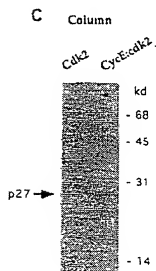
18/32

FIGURE 7B



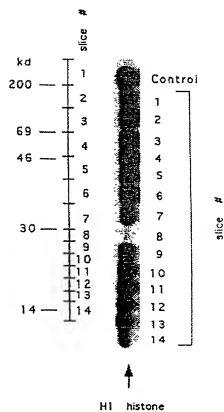
19/32

FIGURE 7C



20/32

FIGURE 7D



21/32

FIGURE 8D

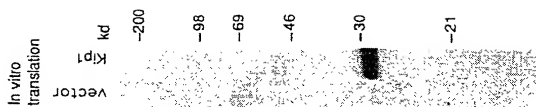


FIGURE 8C

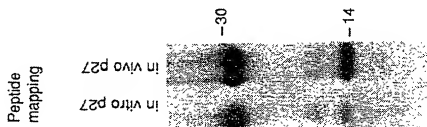


FIGURE 8B

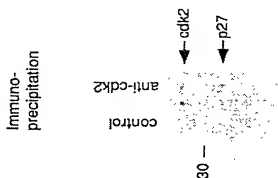
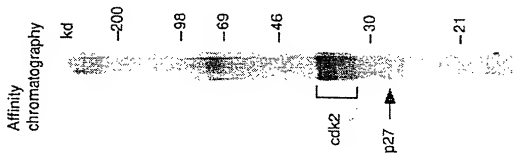


FIGURE 8A



22/32

## FIGURE 9A

mk kipl MSNVRVSNNGSPSLERMDARQAEYKPSACRNLF<sup>20</sup>GGPVNHEELTRDLEKHRR<sup>40</sup>  
 m kipl .....DH.....  
 h kipl .....H.....D.....C.....

mk kipl DMEEASQRKWNFDQNHKPLEGKYEW<sup>70</sup>OEVEKGS<sup>90</sup>SLPEFYVRRPPRPPKGACH  
 m kipl .....R.....S.....  
 h kipl .....

mk kipl VPAQESQDVSGTRQAVPLMGSQANSE<sup>120</sup>DLVDQKTD<sup>140</sup>TADNQAGLAEQCTG  
 m kipl .L.....S.....I.....R.....MP.SS.....P.....  
 h kipl .....S.P.A..I.AP.....P.....PS.S.T.....A.....

mk kipl IRKR<sup>170</sup>PATDDSSPQNK<sup>190</sup>RANRTEENVSDGSXXXXXXXXXXXXXXXXXXXX  
 m kipl M.....AE...S.....PNAGTVEQTPKKPGLRR-QT  
 h kipl .....T.....S.....R.....

## FIGURE 9B

h kipl MSNVRVSNNGSPSLERMDARQAEHPKPSACRNLF<sup>20</sup>GGPVNHEELTRDLEKHRR<sup>40</sup> 11  
 h cipl MSNPAGDVRQNP<sup>20</sup>CGSHACHRLFGPVNHEELTRDLEKHRR<sup>40</sup> 12

h kipl DMEEASQRKWNFDQNHKPLEGKYEW<sup>70</sup>OEVEKGS<sup>90</sup>SLPEFYVRRPPRPPKGACH 111  
 h cipl GCIQEARE<sup>70</sup>RWNFDVETETPLEGDFM<sup>80</sup>ERV<sup>90</sup>RG<sup>100</sup>LCLEKILMLPTGPRRGRDEL 112

h kipl VPAQESQDVSGSRRRLPLIGAPANSE<sup>120</sup>DLVDPKTDPSDSQTGLAEQCAG<sup>140</sup> 113  
 h cipl GGGRRP<sup>120</sup>GTSPALLQGTAEEDHVDLSL<sup>130</sup>SCTLV<sup>140</sup>PRSRGEQAEGRGSPGDSQ<sup>150</sup> 114

h kipl IRKR<sup>170</sup>PATDDSS<sup>180</sup>TQ-NK<sup>190</sup>FANRTEENVSDGSPNAGSVEQTPKKPGLRRRQT\* 115  
 h cipl IRKR<sup>170</sup>Q<sup>180</sup>LSMTDFYH<sup>190</sup>SKRLIFSRRKP\* 116

00865018.052401

23/32

T01250\*8T059860

FIGURE 10A



FIGURE 10C

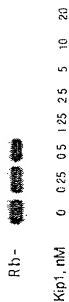


FIGURE 10B

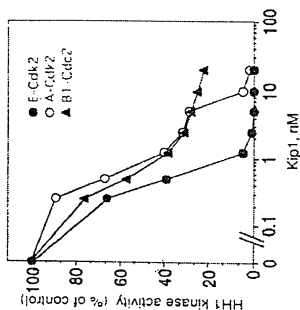
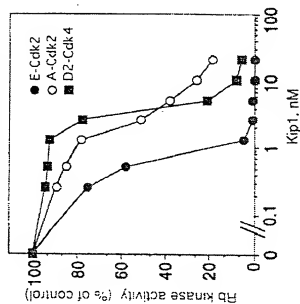
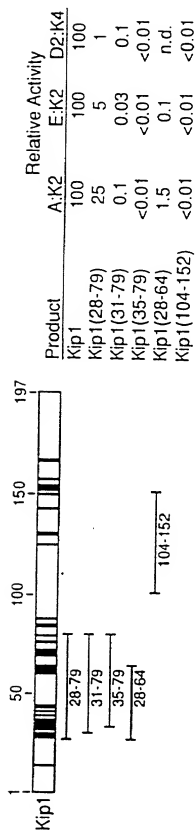


FIGURE 10D



24/32

FIGURE 10E





25/32

FIGURE 11A

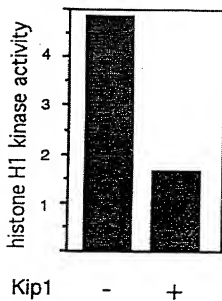


FIGURE 11B



FIGURE 12A

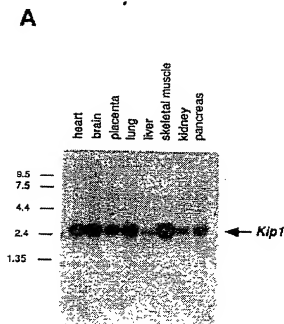
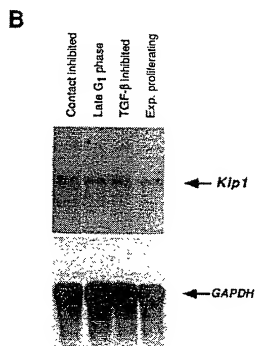


FIGURE 12B



27/32

## FIGURE 13A

ATG TCA AAC GTG CGG GTG TCT AAC GGG AGC CCG AGC CTG GAG CGG ATG Met Ser Asn Val Arg Val Ser Asn Gly Ser Pro Ser Leu Glu Arg Met 1 5 10 15	48
GAC GCC AGA CAG GCG GAG TAC CCC AAG CCC TCC GCC TGC AGA AAC CTC Asp Ala Arg Gln Ala Glu Tyr Pro Lys Pro Ser Ala Cys Arg Asn Leu 20 25 30	96
TTC GGC CCG GTC AAC CAC GAA GAG CTG ACC CGG CAC TTG GAG AAG CAC Phe Gly Pro Val Asn His Glu Glu Leu Thr Arg Asp Leu Glu Lys His 35 40 45	144
CGC AGA GAC ATG GAA GAG GCA AGC CAG CGC ANG TGG AAT TTT GAT TTC Arg Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe 50 55 60	192
CAG AAT CAC AAG CCC CTG GAG GGC AAA TAC GAG TGG CAG GAG GTG GAG Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu 65 70 75 80	240
AAG GGC AGC TTG CCG GAG TTC TAC TAC AGA CCC CCG CGG CCA CCC AAA Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys 85 90 95	288

28/32

104250.87059860

## FIGURE 13B

GGC GGC TGC AAG GTG CCG GCG CAG GAG AGC CAG GAC GTC AGC AGG GGG ACC Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Thr 100 105	336
CGG CAG GCC GTG CCT TTA ATG GGG TCT CAG GCA AAC TCA GAG GAC ACA Arg Gln Ala Val Pro Leu Met Gly Ser Gln Ala Asn Ser Glu Asp Thr 115 120 125	384
CAC TTG GTA GAC CAA AAG ACT GAC AGG GCG GAC AAC CAG GCT GGC TTA His Leu Val Asp Gln Lys Thr Asp Thr Ala Asp Asn Gln Ala Gly Leu 130 135 140	432
GCG GAG CAG TGC ACT GGG ATC AGG AAG CGA CCG GCC ACA GAC GAT TCC Ala Glu Gln Cys Thr Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser 145 150 155 160	480
TCT CCT CAA AAC AAA AGA GCC AAC ACA GAA GAA AAT GTC TCA GAC Ser Pro Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp 165 170 175	528
GGT TCC Gly Ser	534

29/32

FIGURE 14A

ATG TCA AAC GTG AGA GTG TCT AAC GGG AGC CCG AGC CTG GAG CGG ATG Met Ser Asn Val Arg Val Ser Asn Gly Ser Pro Ser Leu Glu Arg Met 1 5 10 15	48
GAC GCC AGA CAA GCG GAT CAC CCC AAG CCT TCC GCC TGC AGA AAT CTC Asp Ala Arg Gln Ala Asp His Pro Lys Pro Ser Ala Cys Arg Asn Leu 20 25 30	96
TTC GGC CCG GTC AAT CAT GAA GAA CTA ACC CCG GAC TTG GAG AAG CAC Phe Gly Pro Val Asn His Glu Glu Leu Thr Arg Asp Leu Glu Lys His 35 40 45	144
TGC CCG GAT ATG GAA GAA GCG AGT CAG CGC AAG TGG AAT TTC GAC TTT Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe 50 55 60	192
CAG AAT CAT AAG CCC CTG GAG GGC AGA TAC GAA TGG CAG GAG GTG GAG Gln Asn His Lys Pro Leu Glu Gly Arg Tyr Glu Trp Gln Glu Val Glu 65 70 75 80	240
AGG GGC AGC TTG CCC GAG TTC TAC TAC AGG CCC CCG CGC CCC CCC AAG Arg Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys 85 90 95	288
AGC GCC TGC AAG GTG CTG GCG CAG GAG AGC CAG GAT GTC AGC GGG AGC Ser Ala Cys Lys Val Leu Ala Gln Glu Ser Gln Asp Val Ser Gly Ser 100 105 110	336

FO4250' 8T059860

30/32

T04250\*8T059860

## FIGURE 14B

CGC CAG GCG GTG CCT TTA ATT GGG TCT CAG GCA AAC TCT GAG GAC CGG Arg Gln Ala Val Pro Leu Ile Gly Ser Gln Ala Asn Ser Glu Asp Arg 115 120 125	384
CAT TTG GTG GAC CAA ATG CCT GAC TCG TCA GAC AAT CAG GCT GGG TTA His Leu Val Asp Gln Met Pro Asp Ser Ser Asp Asn Gln Ala Gly Leu 130 135 140	432
GCG GAG CAG TGT CCA GGG ATG AGG AAG CGA CCT GCT GCA GAA GAT TCT Ala Glu Gln Cys Pro Gly Met Arg Lys Arg Pro Ala Ala Glu Asp Ser 145 150 155 160	480
TCT TCG CAA AAC AAA AGG GCC AAC AGA ACA GAA GAA AAT GTT TCA GAC Ser Ser Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp 165 170 175	528
GGT TCC CCG AAC GCT GGC ACT GTG GAG CAG ACG CCC AAG AAG CCC GGC Gly Ser Pro Asn Ala Gly Thr Val Glu Gln Thr Pro Lys Lys Pro Gly 180 185 190	576
CTT CGA CGC CAG ACG TA Leu Arg Arg Gln Thr 195	594

31/32

FIGURE 15A

ATG TCA AAC GTG CGA GTG TCT AAC GGG AGC CCI AGC CTG GAG CGG ATG	48
Met Ser Asn Val Arg Val Ser Asn Gly Ser Pro Ser Leu Glu Arg Met	15
1	
GAC GCC AGG CAG GCG GAG CAC CCC AAG CCC TCG GCC TGC AGG AAC CTC	96
Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu	30
20	
TTC GGC CCG GTG GAC CAC GAA GAG TTA ACC CCG GAC TTG GAG AAG CAC	144
Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His	45
35	
TGC AGA GAC ATG GAA GAG GCG AGC CAG CGC AGG TGG AAT TTC GAT TTT	192
Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe	60
50	
CAG AAT CAC AAA CCC CTA GAG GGC AGG TAC GAG TGG CAA GAG GTG GAG	240
Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu	80
65	
AAG GGC AGC TTG CCC GAG TTC TAC TAC AGA CCC CCG CGG CCC CCC AAA	288
Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys	95
85	
GGT GGC TGC AAG GTG CCG GCG CAG GAG AGC CAG GAT GTC AGC GGG AGC	336
Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser	110
100	

101250.81059860

32/32

104250.81059860

## FIGURE 15B

CGC CCG GCG CCT TTA ATT GGG GCT CCG GCT AAC TCT GAG GAC ACG Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr 115 120	384
CAT TTG GTG GAC CCA AAG ACT GAT CCG TCG GAC AGC CAG ACG GGG TTA His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu 130 135 140	432
CGG GAG CNA TGC GCA GGA ATA AGG AAG CGA CCT GCA ACC GAC GAT TCT Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser 145 150 155 160	480
TCT ACT CAA AAC AAA AGA GCC AAC AGA ACA GAA GAA AAT GTT TCA GAC Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Gln Asn Val Ser Asp 165 170 175	528
SGT TCC CCA AAT GCC GGT TCT GTG GAG CAG ACG CCC AAG AAG CCT GGC Gly Ser Pro Asn Ala Gly Ser Val Gln Gln Thr Pro Lys Lys Pro Gly 180 185 190	576
CTC AGA AGA CGT CAA ACG TA Leu Arg Arg Arg Gln Thr 195	597